

## SEQUENCE LISTING

<110> Beals, John

Kuchibhotla, Uma

<120> HETEROLOGOUS G-CSF FUSION PROTEINS

<130> P-15648

<160> 66

<170> PatentIn version 3.1

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<212> PRT

<213> Artificial Sequence

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<223> synthetic construct

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<222> (17)..(17)

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<222> (37)..(37)

<223> Xaa at position 37 is Ala or Asn;

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<222> (38)..(38)

<223> Xaa at position 38 is Thr, or any other amino acid exept Pro;

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<222> (39)..(39)

<223> Xaa at position 39 is Tyr, Thr, or Ser;

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<222> (57)..(57)

<223> Xaa at position 57 is Pro or Val;

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<222> (58)..(58)

<223> Xaa at position 58 is Trp or Asn;

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<222> (59)..(59)

<223> Xaa at position 59 is Ala or any other amino acid except Pro;

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<222> (60)..(60)

<223> Xaa at position 60 is Pro, Thr, Asn, or Ser;

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<222> (61)..(61)

<223> Xaa at position 61 is Leu, or any other amino acid except Pro;

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<222> (62)..(62)

<223> Xaa at position 62 is Ser or Thr;

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<222> (63)..(63)

<223> Xaa at position 63 Ser or Asn;

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<222> (64)..(64)

<223> Xaa at position 64 is Cys or any other amino acid except Pro;

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<222> (65)..(65)

<223> Xaa at position 65 is Pro, Ser, or Thr;

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<222> (66) .. (66)

<223> Xaa at position 66 is Ser or Thr;

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<222> (67) .. (67)

<223> Xaa at position 67 is Gln or Asn;

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<222> (68) .. (68)

<223> Xaa at position 68 is Ala or any other amino acid except Pro;

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<221> MISC\_FEATURE

<222> (69) .. (69)

<223> Xaa at position 69 is Leu, Thr, or Ser;

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<222> (93) .. (93)

<223> Xaa at position 93 is Glu or Asn;

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<222> (94) .. (94)

<223> Xaa at position 94 is Gly or any other amino acid except Pro;

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<222> (95)..(95)

<223> Xaa at position 95 is Ile, Asn, Ser, or Thr;

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<222> (97)..(97)

<223> Xaa at position 97 is Pro, Ser, Thr, or Asn;

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<222> (133)..(133)

<223> Xaa at position 133 is Thr or Asn;

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<222> (134)..(134)

<223> Xaa at position 134 is Gln or any other amino acid except Pro;

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<222> (135)..(135)

<223> Xaa at position 135 is Gly, Ser, or Thr;

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<222> (141)..(141)

<223> Xaa at position 141 is Ala or Asn;

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&lt;221&gt; MISC\_FEATURE

&lt;222&gt; (142)..(142)

&lt;223&gt; Xaa at position 142 is Ser or any other amino acid except Pro;

&lt;220&gt;

&lt;221&gt; MISC\_FEATURE

&lt;222&gt; (143)..(143)

&lt;223&gt; Xaa at position 143 is Ala, Ser, or Thr.

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Glu Lys Leu Cys Xaa Xaa Xaa Lys Leu Cys His Pro Glu Glu Leu Val  
35 40 45

Leu Leu Gly His Ser Leu Gly Ile Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa  
50 55 60

Xaa Xaa Xaa Xaa Xaa Gln Leu Ala Gly Cys Leu Ser Gln Leu His Ser  
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Gly Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala Leu Xaa Xaa Xaa Ser  
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Xaa Glu Leu Gly Pro Thr Leu Asp Thr Leu Gln Leu Asp Val Ala Asp  
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Phe Ala Thr Thr Ile Trp Gln Gln Met Glu Glu Leu Gly Met Ala Pro  
115 120 125

Ala Leu Gln Pro Xaa Xaa Xaa Ala Met Pro Ala Phe Xaa Xaa Xaa Phe  
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Gln Arg Arg Ala Gly Gly Val Leu Val Ala Ser His Leu Gln Ser Phe  
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Leu Glu Val Ser Tyr Arg Val Leu Arg His Leu Ala Gln Pro  
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tacggccgga agttgagatg gaagcagcgc cgggcaggag gggtcctggg tgcctcccat     900
ctgcagagct tcgtcgcggc ccgtcctccc caggaccaac ggagggtaga cgtctcgaag     960

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cagaattccg tggaacgggt cggg 1044

<210> 12

<211> 1044

<212> DNA

<213> Artificial Sequence

<220>

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<400> 12

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caattgcgat gggactcgtc gacgcccagc caggccctgc agctggcagg ctgcttgagc 420  
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acactgcagc tggacgtcgc cgacgggctc aaccagggt ggaacctgtg tgacgtcgac 660  
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cagaattccg tggaacgggt cggg 1044



<210> 13

<211> 1044

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic construct

<400> 13

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cagggcgatg ggcagcgct ccagcggaat ctcgttcact ccttctaggt cccgctaccg      180
cgtcgcgagg tcgagaagct gtgtaacacc accaagctgt gccaccccga ggagctgggt      240
ctcttcgaca cattgtgggt gttcgacacg gtggggctcc tcgaccacct gctcggacac      300
tctctgggca tcccctgggc tcccctgagc agctgcgacg agcctgtgac agaccgtag      360
gggacccgag gggactcgtc gacgcccagc aacgccaccc agctggcagg ctgcttgagc      420
caactccata gcgggtcggt gcggtgggtc gaccgtccga cgaactcggg tgaggtatcg      480
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cagaattccg tggaacgggt cggg                                     1044
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<210> 14

<211> 1044

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic construct

<400> 14

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cagggcgatg gcgcagcgct ccagcggaat ctcgttcact ctttctaggt cccgctaccg      180
cgtcgcgagg tcgagaagct gtgtaacacc accaagctgt gccaccccca ggagctgggt      240
ctcttcgaca cattgtgggt gttcgacacg gtggggctcc tcgaccacct gctcggacac      300
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gggacccgag gggactcgtc gacgcccagc caggccctgc agctggcagg ctgcttgagc      420
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cagaattccg tggaacgggt cggg                                     1044
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<210> 15

<211> 1044

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic construct

<400> 15

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cagggcgatg ggcagcgcct ccagcggaaat ctcgttcact ccttctaggt cccgctaccg	180
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cagaattccg tggaacgggt cggg	1044

<210> 16

<211> 1044

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic construct

<400> 16

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cagggcgatg ggcgagcgct ccagcggaat ctcgttcact ccttctaggt cccgctaccg 180  
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ctcttcgaca catttgtgtg gttcgacacg gtggggctcc tcgaccacct gctcggacac 300  
tctctgggca tcccctgggc tcccctgagc aattgcgacg agcctgtgac agaccgtag 360  
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caactccata gctggtcggt ccgggacgtc gaccgtccga cgaactcggg tgaggtatcg 480  
ggccttttcc tctaccaggg gtcctgcag gccctgaacg ggacctcccc ggaaaaggag 540  
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<210> 17

<211> 1762

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic construct

<400> 17

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aaattagtga atgaagtaac tgaatttgca aaaacatgtg ttgctgatga gtcagctgaa 180  
aattgtgaca aatcacttca tacccttttt ggagacaaat tatgcacagt tgcaactctt 240  
cgtgaaacct atggtgaaat ggctgactgc tgtgcaaaac aagaacctga gagaaatgaa 300

tgcttcttgc aacacaaaga tgacaacca aacctcccc gattggtgag accagaggtt 360  
gatgtgatgt gcaactgcttt tcatgacaat gaagagacat ttttgaaaaa atacttatat 420  
gaaattgcc aagacatcc ttacttttat gccccggaac tccttttctt tgctaaaagg 480  
tataaagctg cttttacaga atgttgccaa gctgctgata aagctgcctg cctgttgcca 540  
aagctcgatg aacttcggga tgaagggaag gcttcgtctg ccaaacagag actcaagtgt 600  
gccagtctcc aaaaatttgg agaaagagct ttcaaagcat gggcagtagc tcgcctgagc 660  
cagagatttc ccaaagctga gtttgacaga gtttccaagt tagtgacaga tcttaccaaa 720  
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&lt;210&gt; 18

&lt;211&gt; 232

&lt;212&gt; PRT

<213> Artificial Sequence

<220>

<223> synthetic construct

<400> 18

Ala Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro  
1 5 10 15

Ala Pro Glu Lys Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro  
20 25 30

Lys Asp Thr Lys Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val  
35 40 45

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val  
50 55 60

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln  
65 70 75 80

Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln  
85 90 95

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala  
100 105 110

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro  
115 120 125

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr  
130 135 140

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser  
145 150 155 160

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr  
165 170 175

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr  
180 185 190

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe  
 195 200 205

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys  
 210 215 220

Ser Leu Ser Leu Ser Pro Gly Lys  
 225 230

<210> 19

<211> 229

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic construct

<400> 19

Glu Ser Lys Tyr Gly Pro Pro Cys Pro Pro Cys Pro Ala Pro Glu Phe  
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Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr  
 20 25 30

Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val  
 35 40 45

Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val  
 50 55 60

Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser  
 65 70 75 80

Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu  
 85 90 95

Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ser  
 100 105 110

Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro  
 115 120 125

Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys Asn Gln  
130 135 140

Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala  
145 150 155 160

Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr  
165 170 175

Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu  
180 185 190

Thr Val Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser Cys Ser  
195 200 205

Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser  
210 215 220

Leu Ser Leu Gly Lys  
225

<210> 20

<211> 585

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic construct

<400> 20

Asp Ala His Lys Ser Glu Val Ala His Arg Phe Lys Asp Leu Gly Glu  
1 5 10 15

Glu Asn Phe Lys Ala Leu Val Leu Ile Ala Phe Ala Gln Tyr Leu Gln  
20 25 30

Gln Cys Pro Phe Glu Asp His Val Lys Leu Val Asn Glu Val Thr Glu  
35 40 45



Phe Ala Lys Thr Cys Val Ala Asp Glu Ser Ala Glu Asn Cys Asp Lys  
 50 55 60

Ser Leu His Thr Leu Phe Gly Asp Lys Leu Cys Thr Val Ala Thr Leu  
 65 70 75 80

Arg Glu Thr Tyr Gly Glu Met Ala Asp Cys Cys Ala Lys Gln Glu Pro  
 85 90 95

Glu Arg Asn Glu Cys Phe Leu Gln His Lys Asp Asp Asn Pro Asn Leu  
 100 105 110

Pro Arg Leu Val Arg Pro Glu Val Asp Val Met Cys Thr Ala Phe His  
 115 120 125

Asp Asn Glu Glu Thr Phe Leu Lys Lys Tyr Leu Tyr Glu Ile Ala Arg  
 130 135 140

Arg His Pro Tyr Phe Tyr Ala Pro Glu Leu Leu Phe Phe Ala Lys Arg  
 145 150 155 160

Tyr Lys Ala Ala Phe Thr Glu Cys Cys Gln Ala Ala Asp Lys Ala Ala  
 165 170 175

Cys Leu Leu Pro Lys Leu Asp Glu Leu Arg Asp Glu Gly Lys Ala Ser  
 180 185 190

Ser Ala Lys Gln Arg Leu Lys Cys Ala Ser Leu Gln Lys Phe Gly Glu  
 195 200 205

Arg Ala Phe Lys Ala Trp Ala Val Ala Arg Leu Ser Gln Arg Phe Pro  
 210 215 220

Lys Ala Glu Phe Ala Glu Val Ser Lys Leu Val Thr Asp Leu Thr Lys  
 225 230 235 240

Val His Thr Glu Cys Cys His Gly Asp Leu Leu Glu Cys Ala Asp Asp  
 245 250 255

Arg Ala Asp Leu Ala Lys Tyr Ile Cys Glu Asn Gln Asp Ser Ile Ser  
 260 265 270

Ser Lys Leu Lys Glu Cys Cys Glu Lys Pro Leu Leu Glu Lys Ser His  
 275 280 285

Cys Ile Ala Glu Val Glu Asn Asp Glu Met Pro Ala Asp Leu Pro Ser  
 290 295 300

Leu Ala Ala Asp Phe Val Glu Ser Lys Asp Val Cys Lys Asn Tyr Ala  
 305 310 315 320

Glu Ala Lys Asp Val Phe Leu Gly Met Phe Leu Tyr Glu Tyr Ala Arg  
 325 330 335

Arg His Pro Asp Tyr Ser Val Val Leu Leu Leu Arg Leu Ala Lys Thr  
 340 345 350

Tyr Glu Thr Thr Leu Glu Lys Cys Cys Ala Ala Ala Asp Pro His Glu  
 355 360 365

Cys Tyr Ala Lys Val Phe Asp Glu Phe Lys Pro Leu Val Glu Glu Pro  
 370 375 380

Gln Asn Leu Ile Lys Gln Asn Cys Glu Leu Phe Glu Asn Leu Gly Glu  
 385 390 395 400

Tyr Lys Phe Gln Asn Ala Leu Leu Val Arg Tyr Thr Lys Lys Val Pro  
 405 410 415

Gln Val Ser Thr Pro Thr Leu Val Glu Val Ser Arg Asn Leu Gly Lys  
 420 425 430

Val Gly Ser Lys Cys Cys Lys His Pro Glu Ala Lys Arg Met Pro Cys  
 435 440 445

Ala Glu Asp Tyr Leu Ser Val Val Leu Asn Gln Leu Cys Val Leu His  
 450 455 460

Glu Lys Thr Pro Val Ser Asp Arg Val Thr Lys Cys Cys Thr Glu Ser  
 465 470 475 480

Leu Val Asn Arg Arg Pro Cys Phe Ser Ala Leu Glu Val Asp Glu Thr  
 485 490 495

Tyr Val Pro Lys Glu Phe Asn Ala Glu Thr Phe Thr Phe His Ala Asp  
 500 505 510

Ile Cys Thr Leu Ser Glu Lys Glu Arg Gln Ile Lys Lys Gln Thr Ala  
 515 520 525

Leu Val Glu Leu Val Lys His Lys Pro Lys Ala Thr Lys Glu Gln Leu  
 530 535 540

Lys Ala Val Met Asp Asp Phe Ala Ala Phe Val Glu Lys Cys Cys Lys  
 545 550 555 560

Ala Asp Asp Lys Glu Thr Cys Phe Ala Glu Glu Gly Lys Lys Leu Val  
 565 570 575

Ala Ala Ser Gln Ala Ala Leu Gly Leu  
 580 585

<210> 21

<211> 703

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic construct

<400> 21

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acccttgagg	tcacatgcgt	ggtggtggac	gtgagccacg	aagaccctga	ggtcaagttc	180
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aggtggcagc	aggggaacgt	cttctcatgc	tccgtgatgc	atgaggctct	gcacaaccac	660
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<210> 22

<211> 981

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic construct

<400> 22

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caggtcagcc tgacctgct ggtcaaaggc ttctacccca gcgacatcgc cgtggagtgg	780
gagagcaatg ggcagccgga gaacaactac aagaccacgc ctcccgtgct ggactccgac	840
ggctccttct tcctctacag caggctaacc gtggacaaga gcaggtggca ggaggggaat	900
gtcttctcat gctccgtgat gcatgaggct ctgcacaacc actacacaca gaagagcctc	960
tcctgtctc tgggtaaatg a	981

<210> 23

<211> 406

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic construct

<400> 23

Thr Pro Leu Gly Pro Ala Ser Ser Leu Pro Gln Ser Phe Leu Leu Lys  
1 5 10 15

Ala Leu Glu Gln Val Arg Lys Ile Gln Gly Asp Gly Ala Ala Leu Gln  
20 25 30

Glu Lys Leu Cys Ala Thr Tyr Lys Leu Cys His Pro Glu Glu Leu Val  
35 40 45

Leu Leu Gly His Ser Leu Gly Ile Pro Trp Ala Pro Leu Ser Ser Cys  
50 55 60

Pro Ser Gln Ala Leu Gln Leu Ala Gly Cys Leu Ser Gln Leu His Ser  
65 70 75 80

Gly Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala Leu Glu Gly Ile Ser  
85 90 95

Pro Glu Leu Gly Pro Thr Leu Asp Thr Leu Gln Leu Asp Val Ala Asp  
100 105 110

Phe Ala Thr Thr Ile Trp Gln Gln Met Glu Glu Leu Gly Met Ala Pro  
115 120 125

Ala Leu Gln Pro Thr Gln Gly Ala Met Pro Ala Phe Ala Ser Ala Phe  
130 135 140

Gln Arg Arg Ala Gly Gly Val Leu Val Ala Ser His Leu Gln Ser Phe  
145 150 155 160

Leu Glu Val Ser Tyr Arg Val Leu Arg His Leu Ala Gln Pro Glu Pro  
165 170 175

Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu  
180 185 190

Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp  
 195 200 205

Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp  
 210 215 220

Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly  
 225 230 235 240

Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn  
 245 250 255

Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp  
 260 265 270

Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro  
 275 280 285

Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu  
 290 295 300

Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn  
 305 310 315 320

Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile  
 325 330 335

Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr  
 340 345 350

Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys  
 355 360 365

Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys  
 370 375 380

Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu  
 385 390 395 400

Ser Leu Ser Pro Gly Lys  
 405

&lt;211&gt; 403

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; synthetic construct

&lt;400&gt; 24

Thr Pro Leu Gly Pro Ala Ser Ser Leu Pro Gln Ser Phe Leu Leu Lys  
1 5 10 15

Ala Leu Glu Gln Val Arg Lys Ile Gln Gly Asp Gly Ala Ala Leu Gln  
20 25 30

Glu Lys Leu Cys Ala Thr Tyr Lys Leu Cys His Pro Glu Glu Leu Val  
35 40 45

Leu Leu Gly His Ser Leu Gly Ile Pro Trp Ala Pro Leu Ser Ser Cys  
50 55 60

Pro Ser Gln Ala Leu Gln Leu Ala Gly Cys Leu Ser Gln Leu His Ser  
65 70 75 80

Gly Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala Leu Glu Gly Ile Ser  
85 90 95

Pro Glu Leu Gly Pro Thr Leu Asp Thr Leu Gln Leu Asp Val Ala Asp  
100 105 110

Phe Ala Thr Thr Ile Trp Gln Gln Met Glu Glu Leu Gly Met Ala Pro  
115 120 125

Ala Leu Gln Pro Thr Gln Gly Ala Met Pro Ala Phe Ala Ser Ala Phe  
130 135 140

Gln Arg Arg Ala Gly Gly Val Leu Val Ala Ser His Leu Gln Ser Phe  
145 150 155 160

Leu Glu Val Ser Tyr Arg Val Leu Arg His Leu Ala Gln Pro Glu Ser  
165 170 175

Lys Tyr Gly Pro Pro Cys Pro Ser Cys Pro Ala Pro Glu Phe Leu Gly  
 180 185 190

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met  
 195 200 205

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser Gln  
 210 215 220

Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val  
 225 230 235 240

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr  
 245 250 255

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly  
 260 265 270

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile  
 275 280 285

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val  
 290 295 300

Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser  
 305 310 315 320

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu  
 325 330 335

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro  
 340 345 350

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val  
 355 360 365

Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met  
 370 375 380

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser  
 385 390 395 400

Leu Gly Lys



&lt;210&gt; 25

&lt;211&gt; 500

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; synthetic construct

&lt;400&gt; 25

Thr Pro Leu Gly Pro Ala Ser Ser Leu Pro Gln Ser Phe Leu Leu Lys  
1 5 10 15

Ala Leu Glu Gln Val Arg Lys Ile Gln Gly Asp Gly Ala Ala Leu Gln  
20 25 30

Glu Lys Leu Cys Ala Thr Tyr Lys Leu Cys His Pro Glu Glu Leu Val  
35 40 45

Leu Leu Gly His Ser Leu Gly Ile Pro Trp Ala Pro Leu Ser Ser Cys  
50 55 60

Pro Ser Gln Ala Leu Gln Leu Ala Gly Cys Leu Ser Gln Leu His Ser  
65 70 75 80

Gly Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala Leu Glu Gly Ile Ser  
85 90 95

Pro Glu Leu Gly Pro Thr Leu Asp Thr Leu Gln Leu Asp Val Ala Asp  
100 105 110

Phe Ala Thr Thr Ile Trp Gln Gln Met Glu Glu Leu Gly Met Ala Pro  
115 120 125

Ala Leu Gln Pro Thr Gln Gly Ala Met Pro Ala Phe Ala Ser Ala Phe  
130 135 140

Gln Arg Arg Ala Gly Gly Val Leu Val Ala Ser His Leu Gln Ser Phe  
145 150 155 160

Leu Glu Val Ser Tyr Arg Val Leu Arg His Leu Ala Gln Pro Gly Gly  
165 170 175

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ala His  
180 185 190

Lys Ser Glu Val Ala His Arg Phe Lys Asp Leu Gly Glu Glu Asn Phe  
195 200 205

Lys Ala Leu Val Leu Ile Ala Phe Ala Gln Tyr Leu Gln Gln Cys Pro  
210 215 220

Phe Glu Asp His Val Lys Leu Val Asn Glu Val Thr Glu Phe Ala Lys  
225 230 235 240

Thr Cys Val Ala Asp Glu Ser Ala Glu Asn Cys Asp Lys Ser Leu His  
245 250 255

Thr Leu Phe Gly Asp Lys Leu Cys Thr Val Ala Thr Leu Arg Glu Thr  
260 265 270

Tyr Gly Glu Met Ala Asp Cys Cys Ala Lys Gln Glu Pro Glu Arg Asn  
275 280 285

Glu Cys Phe Leu Gln His Lys Asp Asp Asn Pro Asn Leu Pro Arg Leu  
290 295 300

Val Arg Pro Glu Val Asp Val Met Cys Thr Ala Phe His Asp Asn Glu  
305 310 315 320

Glu Thr Phe Leu Lys Lys Tyr Leu Tyr Glu Ile Ala Arg Arg His Pro  
325 330 335

Tyr Phe Tyr Ala Pro Glu Leu Leu Phe Phe Ala Lys Arg Tyr Lys Ala  
340 345 350

Ala Phe Thr Glu Cys Cys Gln Ala Ala Asp Lys Ala Ala Cys Leu Leu  
355 360 365

Pro Lys Leu Asp Glu Leu Arg Asp Glu Gly Lys Ala Ser Ser Ala Lys  
370 375 380

Gln Arg Leu Lys Cys Ala Ser Leu Gln Lys Phe Gly Glu Arg Ala Phe  
385 390 395 400

Lys Ala Trp Ala Val Ala Arg Leu Ser Gln Arg Phe Pro Lys Ala Glu  
 405 410 415

Phe Ala Glu Val Ser Lys Leu Val Thr Asp Leu Thr Lys Val His Thr  
 420 425 430

Glu Cys Cys His Gly Asp Leu Leu Glu Cys Ala Asp Asp Arg Ala Asp  
 435 440 445

Leu Ala Lys Tyr Ile Cys Glu Asn Gln Asp Ser Ile Ser Ser Lys Leu  
 450 455 460

Lys Glu Cys Cys Glu Lys Pro Leu Leu Glu Lys Ser His Cys Ile Ala  
 465 470 475 480

Glu Val Glu Asn Asp Glu Met Pro Ala Asp Leu Pro Ser Leu Ala Ala  
 485 490 495

Asp Phe Val Glu  
 500

<210> 26

<211> 69

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic construct

<400> 26

gtaagcttgc gtcgacgcta gcggcgcgcc gccatggccg gacctgccac ccagagcccc 60

atgaagctg 69

<210> 27

<211> 61

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic construct

<400> 27

ggggcagggga gctggctggg cccagtggag tggcttctctg cactgtccag agtgcactgt 60

g 61

<210> 28

<211> 59

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic construct

<400> 28

ggacagtgca ggaagccact ccactggggc cagccagctc cctgccccag agcttctctg 59

<210> 29

<211> 72

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic construct

<400> 29

gaacctcgag gatcctcatt agggctgggc aaggtgcctt aagacgcggt acgacacctc 60

caggaagctc tg 72

<210> 30

<211> 69

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic construct

<400> 30

gtaagcttgc gtcgacgcta gcggcgcgcc gccatggccg gacctgccac ccagagcccc 60

atgaagctg 69

<210> 31

<211> 57

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic construct

<400> 31

gctctaaggc cttgagcagg aagctctggg gcagggagct cgctgggccc agtggag 57

<210> 32

<211> 53

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic construct

<400> 32

gggcccagcg agctccctgc ccagagctt cctgctcaag gccttagagc aag 53

<210> 33

<211> 72

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic construct

<400> 33

gaacctcgag gatcctcatt agggctgggc aaggtgcctt aagacgcggt acgacacctc 60

caggaagctc tg 72

<210> 34

<211> 69

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic construct

<400> 34

gtaagcttgc gtcgacgcta gcggcgcgcc gccatggccg gacctgccac ccagagcccc 60

atgaagctg 69

<210> 35

<211> 61

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic construct

<400> 35

gtccgagcag cactagttcc tcggggtggc acagcttggt ggtgttacac agcttctcct 60

g 61

<210> 36

<211> 66

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic construct

<400> 36

ggcgcagcgc tccaggagaa gctgtgtaac accaccaagc tgtgccaccc cgaggaacta 60

gtgctg 66

<210> 37

<211> 72

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic construct

<400> 37

gaacctcgag gacccattc attagggtgggc aaggtgcctt aagacgcggt acgacacctc 60

caggaagctc tg 72

<210> 38

<211> 69

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic construct

<400> 38

gtaagcttgc gtcgacgcta gcggcgcgcc gccatggccg gacctgccac ccagagcccc 60

atgaagctg 69

<210> 39

<211> 61

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic construct

<400> 39

gccccggcgct ggaaagcgct ggcgaaggcc ggcattggcgg tctgggtggg ctgcagggca 60

g 61

<210> 40

<211> 60

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic construct

<400> 40

ggccccctgcc ctgcagccca accagaccgc catgccggcc ttgccagcg ctttccagcg 60

<210> 41

<211> 72

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic construct

<400> 41

gaacctcgag gatcctcatt agggctgggc aaggcgcctt aagacgcggt acgacacctc 60

caggaagctc tg 72

<210> 42

<211> 69

<212> DNA



<213> Artificial Sequence

<220>

<223> synthetic construct

<400> 42

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atgaagctg 69

<210> 43

<211> 68

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic construct

<400> 43

gccccgcgct ggaaggtaga gttgaaggcc ggcattggcac cctgggtggg ctgaagagca 60

ggggccat 68

<210> 44

<211> 74

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic construct

<400> 44

gggaatggcc cctgctcttc agcccaccca gggtgccatg ccggccttca actctacctt 60

ccagcgccgg gcag 74

<210> 45

<211> 72

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic construct

<400> 45  
gaacctcgag gatcctcatt agggctgggc aaggtgcctt aagacgcggt acgacacctc 60  
caggaagctc tg 72

<210> 46

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic construct

<400> 46  
gctagcggcg cgccaccatg 20

<210> 47

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic construct

<400> 47  
gctcagggta gcgttaacga tgcccagaga gtg 33

<210> 48

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic construct

<400> 48

gggcacgcgtt aacgctaccc tgagcagctg

30

<210> 49

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic construct

<400> 49

gactcgagga tcctcattag ggctggg

27

<210> 50

<211> 38

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic construct

<400> 50

gctagcggcg cgccaccatg gccggacctg ccacccag

38

<210> 51

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic construct

<400> 51

caagcagccg gccagctggg tggcggtgct ggggcagctg ctcag

45

<210> 52

<211> 37

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic construct

<400> 52

gccccagcaa cgccaccag ctggccggct gcttgag

37

<210> 53

<211> 47

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic construct

<400> 53

gactcgagga tcctcattag ggctgggcaa ggtgccttaa gacgcgg

47

<210> 54

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic construct

<400> 54  
gctagcggcg cgccaccatg 20

<210> 55

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic construct

<400> 55  
ggggcaacta gtcaggttag cccaggg 27

<210> 56

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic construct

<400> 56  
gctaacctga ctagttgcc cagccag 27

<210> 57

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic construct

<400> 57  
gactcgagga tcctcattag ggctggg 27

<210> 58

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic construct

<400> 58

gctagcggcg cgccaccatg

20

<210> 59

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic construct

<400> 59

ggtgcaattg ctcaggggag cccag

25

<210> 60

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic construct

<400> 60

gcaattgcac cagccaggcc ctg

23

<210> 61

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic construct

<400> 61

gactcgagga tcctcattag ggctggg

27

<210> 62

<211> 38

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic construct

<400> 62

gctagcggcg cgccaccatg gccggacctg ccacccag

38

<210> 63

<211> 37

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic construct

<400> 63

ccggactggg cccgttcagg gcctgcagga gcccctg

37

<210> 64

<211> 35

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic construct

<400> 64

gaacgggacc agtccggagt tgggtccac cttgg

35

<210> 65

<211> 47

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic construct

<400> 65

gactcgagga tcctcattag ggctgggcaa ggtgccttaa gacgcgg

47

<210> 66

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic construct

<400> 66

gtcgacgcta gcggcgcgcc accatggccg gacctg

36